

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:48:45 ; Search time 22.1455 Seconds
(without alignments)
1133.013 Million cell updates/sec

Title: US-09-988-971-2

Perfect score: 1351

Sequence: 1 MSLSPRRKSLPSPSLSSSV.....RESLSPYISLNDVAVSLDA 261

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	497.5	36.8	281	2 A57152	src-like adaptor p
2	374.5	27.7	512	1 TVHULY	protein-tyrosine k
3	371.5	27.5	512	1 I56160	protein-tyrosine k
4	371.5	27.5	512	1 A39719	protein-tyrosine k
5	364.5	27.0	505	1 TVHHC	protein-tyrosine k
6	357.5	26.5	503	1 J01321	protein-tyrosine k
7	356.5	26.4	505	2 I37206	protein-tyrosine k
8	356.5	26.4	503	1 TVM5HC	protein-tyrosine k
9	348.5	25.8	499	1 A40092	protein-tyrosine k
10	344.5	25.5	509	1 OKHULK	protein-tyrosine k
11	342.5	25.4	509	1 I48845	protein-tyrosine k
12	337.5	24.9	507	1 A39939	protein-tyrosine k
13	329.5	24.4	539	2 B49114	protein-tyrosine k
14	324.5	24.0	528	1 TVPVG9	protein-tyrosine k
15	323.5	23.9	537	1 A45501	protein-tyrosine k
16	321.5	23.8	541	1 TVCHXS	protein-tyrosine k
17	319.5	23.6	537	1 TVHUSY	protein-tyrosine k
18	319.5	23.6	543	1 TVHUSY	protein-tyrosine k
19	316.5	23.4	529	1 TVHUF8	protein-tyrosine k
20	315.5	23.3	544	2 I51593	protein-tyrosine k
21	314.5	23.3	537	1 A43806	protein-tyrosine k
22	313.5	23.2	534	1 A44991	protein-tyrosine k
23	311.5	23.0	517	2 S24547	protein-tyrosine k
24	309.5	22.9	537	2 I51592	protein-tyrosine k
25	309.5	22.9	541	2 S31445	protein-tyrosine k
26	305.5	22.6	517	2 A43807	protein-tyrosine k
27	305.5	22.6	536	2 S33569	protein-tyrosine k
28	301.5	22.3	534	2 S33568	protein-tyrosine k
29	299.5	22.2	542	2 A49114	protein-tyrosine k

30	294.5	21.8	506	1 S24553	protein-tyrosine k
31	290.5	21.5	557	1 TVFVS2	protein-tyrosine k
32	290.5	21.5	587	1 TVFVPR	protein-tyrosine k
33	288.5	21.4	533	1 TVCHS	protein-tyrosine k
34	288.5	21.4	568	1 TVFVSL	protein-tyrosine k
35	283.5	21.0	526	1 TVFV60	protein-tyrosine k
36	280.5	20.7	509	1 TVHAST	protein-tyrosine k
37	279.5	20.7	546	2 S52314	protein-tyrosine k
38	278.5	20.6	532	1 B34104	protein-tyrosine k
39	277.5	20.5	526	1 TVFVR	protein-tyrosine k
40	277.5	20.5	526	2 S15582	protein-tyrosine k
41	277.5	20.5	542	1 TVHUSC	protein-tyrosine k
42	277.5	20.5	545	2 S52313	protein-tyrosine k
43	276.5	20.4	541	1 A43610	protein-tyrosine k
44	275.5	20.4	532	1 A34104	protein-tyrosine k
45	273.5	20.2	526	2 S24520	protein-tyrosine k

ALIGNMENTS

RESULT 1
A57152
src-like adaptor protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 12-Feb-1999
C/Accession: A57152
J. Pandey, A.; Duan, H.; Dixit, V.M.
J. Biol. Chem. 270, 19201-19204, 1995
A/Title: Characterization of a novel Src-like adaptor protein that associates with the F
A/Reference number: A57152; MUID:95370243; PMID:7543898
A/Accession: A57152
A/status: preliminary; not compared with conceptual translation
A/molecule type: mRNA
A/residues: 1-281 <P>N>
A/cross-references: GB:U29056
F.29-77/Domain: SH3 homology; SH2 homology
F.84-175/Domain: SH2 homology <SH2>

Query Match	36.8%	Score 497.5;	DB 2;	Length 281;
Best Local Similarity	43.9%	Pred. No. 1.4e-33;		
Matches 116;	Conservative 38;	Mismatches 81;	Indels 29;	Gaps 7;
QY	9 KSLSPSPS---	SSSVGQGPVTMEARSRKATVALGSPGPAELSLTSGPLTVISD 65		
DB	6 KSTSPSPSPS---	EGLESDPLAV-LITPESDISPIFRGKRLRVISDE 55		
QY	66 GDMWTVLSEVSGREYNISVAVAKSHGWLVEGLSREKAEELLPLFGNGAPLIRISQT 125			
DB	56 GGMWKAISLSTRESYIPGICVARVYHGLFEGLRKAEELLQLPDTKIGSPMIRRESST 115			
QY	126 RRGYSIVRLRPAWMDRIHRIHCLDNGWLYISPLTFPSLOALVDHYSELADIC 185			
DB	116 KKGYSIVSR-----	HRQVGHYRIFRLPMNMYISRLTLFQGLLELVTHYSEVADGCC 169		
QY	186 LMEPCVDR-----	AGPLPGKDIPLPTVQRTPLNKEIDSSLFSEPAAG---EESL 236		
DB	170 VLTPLCAQINAPTPSPSPCTSPGSPVTLRKTFDKWRKVRSLQEGSBECAENPLRVDESL 229			
QY	237 LSEGLRESLSPYISL-NDEAVSLD 259			
DB	230 FSYGLRESIASVLSLTGDDSSFD 253			

RESULT 2
TVHULY
protein-tyrosine kinase (EC 2.7.1.112) 1Yn, splice form A - human
N/Contains: protein-tyrosine kinase 1Yn, splice form B
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 18-Feb-2000
C/Accession: A26719; D38268; P09499; I53715
R.Yamashita, Y.; Fukushige, S.I.; Semba, K.; Sukegawa, J.; Miyajima, N.; Matsubara, K.;

R.Stanley, E.; Ralph, S.; McEwen, S.; Boulet, I.; Holtzman, D.A.; Lock, P.; Dunn, A.R.
 Mol. Cell. Biol. 11, 3399-3406, 1991
 A>Title: Alternatively spliced murine lyn mRNAs encode distinct proteins.
 A.Reference number: A39719; MUID:91260688; PMID:1710766
 A.Accession: A39719
 A.Molecule type: mRNA
 A.Residues: 1-512 <STA>
 A.Cross-references: GB:M64608; NID:g198938; PIDN:AAA3470.1; PID:g198939
 A.Accession: B39719
 A.Molecule type: mRNA
 A.Residues: 1-24, 46-512 <STA2>
 A.Cross-references: GB:M64608
 R.Yi, T.; Boelen, J.B.; Inle, J.N.
 Mol. Cell. Biol. 11, 2391-2398, 1991
 A>Title: Hematopoietic cells express two forms of lyn kinase differing by 21 amino acids
 A.Reference number: A39750; MUID:91203857; PMID:2017160
 A.Accession: A39750
 A.Molecule type: mRNA
 A.Residues: 1-76, 'F', 78-160, 'I', 162-278, 'L', 280-390, 'I', 392-424, 'D', 426-512 <Y11>
 A.Cross-references: GB:M57696; NID:g198940; PIDN:AAA3471.1; PID:g198941
 A.Accession: B39750
 A.Molecule type: mRNA
 A.Residues: 1-24, 46-76, 'F', 78-160, 'I', 162-278, 'L', 280-390, 'I', 392-424, 'D', 426-512 <Y12>
 A.Cross-references: GB:M57697; NID:G198942; PIDN:AAA3472.1; PID:g198943
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH3 h
 C:Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotein
 F1-512/Product: protein-tyrosine kinase lyn, long splice form #status predicted <MATL>
 F1-74, 46-512/Product: protein-tyrosine kinase lyn, short splice form #status predicted
 F120-118/Domain: SH3 homology <SH3>
 F129-226/Domain: SH2 homology <SH2>
 F245-504/Domain: protein kinase homology <KIN>
 F253-261/Region: protein kinase ATP-binding motif
 F12/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F1275/Active site: Lys #status predicted
 F1397/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 27.5%; Score 371.5; DB 1; Length 512;
 Best Local Similarity 40.8%; Pred. No. 7, 46-23;
 Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;

Qy 6 SRRKSLSPSSLSVQGGPVTMEARSKATVVALGSPGAPAEISLRLGEPPLTVSDD 65
 Db 38 SNKQRPVPER-HILPGORFOTKDPBEGDITVALYPPDGIHPDLSFFKSGKKVLEEH 96
 Qy 66 GDMWTVLSEVSGREYNIPSVHAKV-----SHQWLYEGLSREKAEELLPLPGPGAFILIR 121
 Db 97 GEMWAKSLSSKREGFIPSNVAKVNTLETMEWPFKQITRKDAERQLAPGSAAGAFILIR 156
 Qy 122 ESOTRRGSYSLSVLRSPASMDRIHRYRICHLDNGMGLYISPRLTSPSLDALVDHYSELAD 181
 Db 157 ESETLKGSFSLSVRYDPMHGDVYIKHKKIRSLDNGGYISPRITPCISDMIKHYKQSD 216
 Qy 182 DICLLKEPCVLQRAAPLPCK 202
 Db 217 GLCRLEKACI-----SPKPK 233

RESULT 5
 TVHHC
 protein-tyrosine kinase (EC 2.7.1.112) hck - human
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1989 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
 C:Accession: A27811; J01149; C38268; S31103
 R:Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, M.M.; Die
 Mol. Cell. Biol. 7, 2267-2275, 1987
 A>Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and
 A.Reference number: A27811; MUID:87257942; PMID:3496523
 A.Accession: A27811
 A.Molecule type: mRNA
 A.Residues: 1-505 <QUT>
 A.Cross-references: GB:M16591
 A>Note: the codon given for 3-Cys (TCG) is inconsistent with the authors' translation
 R.Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M.

Mol. Cell. Biol. 7, 2276-2285, 1987
 A>Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of h
 A.Reference number: A27812; MUID:87257943; PMID:3453117
 A.Accession: A27812
 A.Molecule type: mRNA
 A.Residues: 1-505 <ZIR>
 A.Cross-references: GB:M16592; NID:g183913; PIDN:AAA52644.1; PID:g306833
 R.Hildebrand, D.; Scherhardt, K.; Ruebsamen-Waismann, H.
 Gene 113, 275-280, 1992
 A>Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinase
 A.Reference number: J01149; MUID:92241680; PMID:1572549
 A.Accession: J01149
 A.Molecule type: DNA
 A.Residues: 157-505 <HRA>
 A.Cross-references: EMBL:X59741
 R.Parten, U.; Maekela, T.P.; Altalo, R.; Lehtvaesaho, H.; Altalo, K.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
 A>Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
 A.Reference number: A38268; MUID:91062389; PMID:2247464
 A.Accession: C38268
 A>Status: nucleic acid sequence not shown; not compared with conceptual translation
 A.Molecule type: mRNA
 A.Residues: 362-417 <PAR>
 C:Genetics:
 A:Gene: GDB:HCK
 A:Cross-references: GDB:119303; OMIM:142370
 A:Map position: 20q11-20q12
 A:Introns: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1
 C:Function:
 A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH3 h
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
 F1-505/Product: protein-tyrosine kinase hck #status predicted <MAT>
 F164-112/Domain: SH3 homology <SH3>
 F123-220/Domain: SH2 homology <SH2>
 F1239-497/Domain: protein kinase homology <KIN>
 F1247-255/Region: protein kinase ATP-binding motif
 F12/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F123/Binding site: palmitate (Cys) (covalent) #status predicted
 F1268/Active site: Lys #status predicted
 F1390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 27.0%; Score 364.5; DB 1; Length 505;
 Best Local Similarity 42.2%; Pred. No. 2, 76-22;
 Matches 78; Conservative 31; Mismatches 69; Indels 7; Gaps 2;

Qy 12 PPSLSVSSVQGGPVTMEARSKATVVALGSPGAPAEISLRLGEPPLTVSDDGWTV 71
 Db 40 PGNSHNS--NTGIREAGSEDIIVVALYDEAIHHEDLSFQKDDQVWVLESGEWMXA 96
 Qy 72 LSEVSGREYNIPSVHAKV-----SHQWLYEGLSREKAEELLPLPGPGAFILIR 127
 Db 97 RSLATRKSGYIPSNVAVRVDLSLETMEWPFKISKDAERQLAPGNMGLSFWIRDEETIK 156
 Qy 128 GSYSLSVLRSPASMDRIHRYRICHLDNGMGLYISPRLTSPSLDALVDHYSELADICLL 187
 Db 157 GSYSLSVLRDVPDQGVTVHRYKIRLIDNGGYISPRSTLQELVDHYKKGNDGCOPL 216
 Qy 188 KEPCV 192
 Db 217 SVPCM 221

RESULT 6
 J01321
 protein-tyrosine kinase (EC 2.7.1.112) hck - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: J01321; S18974
 R:Okano, Y.; Sugimoto, Y.; Fukuko, M.; Matsui, A.; Negata, K.; Nozawa, Y.
 Biochem. Biophys. Res. Commun. 181, 1137-1144, 1991
 A>Title: Identification of rat cDNA encoding hck tyrosine kinase from megakaryocytes.
 A.Reference number: J01321; MUID:92109719; PMID:1764064

[illegible]

Qy 186 ICCLKEPCVLQKAPGLPGK 202
Db 210 LQQLSVPCV-----SPKPK 225

RESULT 9

protein-tyrosine kinase (EC 2.7.1.112) blk [validated] - mouse

C:Species: Mus musculus (house mouse)

C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000

C:Accession: A40092

R:Dymectil, S.M.; Niederhuber, J.E.; Desiderio, S.V.

Science 247, 332-336, 1990

A>Title: Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.

A:Reference number: A40092; MUID:90117147; PMID:2404338

A:Accession: A40092

A:Molecule type: mRNA

A:Residues: 1-499 <DYM>

A:Cross-references: GB:M0903; NID:g202076; PIDN:AAA40453.1; PID:g202077

C:Gene: MGI:Blk

A:Cross-references: MGI:88169

A:Map position: 14:28.0

C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pnc

F:118-214/Domain: SH2 homology <SH2>

F:241-249/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:263/Active site: Lys #status predicted

Query Match 25.8%; Score 348.5; DB 1; Length 499;

Best Local Similarity 36.5%; Pred. No. 5.66-21;

Matches 81; Conservative 32; Mismatches 72; Indels 37; Gaps 4;

Qy 1 MGLSSRKSLSPLSSVGGQPV-----TMEERSK 34

Db 1 MGLSSRKS-----VSEKSGKSPVIRITQKAPPLPLVFNHLPSPDNDPDEE 54

Qy 35 ATAVAGSPAGPAELSLRLGEPLTIVSEGDPMWTVLSEVSEVNPVAVAKVS--- 91

Db 55 RFVVALPDVAANVDRDLQVLKGEGLQVLSSTGDMWLSLVTEGEGVSNVAVEYLE 114

Qy 92 -HGMVLEGLSRKAEELLLDGNCGAFILRSQTRRSYSLRSLRSPASWDRIHRYI 150

Db 115 VEKFFETISRKDAERQLLAPMNAQGFILRSSESNKGAFLSVK-DITTOGEVVKHYKI 173

Qy 151 HCLDNGMLYISPLTLPSTLQALVDHSELDADDICCLKEPCV 192

Db 174 RSLDNGGYISPLTLPSTLQALVDHSELDADDICCLKEPCV 215

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

A:Molecule type: mRNA

A:Residues: 1-86; P, 88-509 <PER>

A:Cross-references: EMBL:X1529; NID:g34294; PIDN:CAA31884.1; PID:g34295

R:Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikawa, Y.; Mak, T.W.

Eur. J. Immunol. 16, 1643-1646, 1986

A>Title: A human T cell-specific cDNA clone (Y116) encodes a protein with extensive homology

A:Reference number: S07200; MUID:87133831; PMID:3493153

A:Accession: S07200

A:Molecule type: mRNA

A:Residues: 1-205; ASALPT, 212-257, 'RCGW', 262, 'TTT', 266, 'T', 268-281, 'AGRLP', 287-503, 'ST

A:Cross-references: EMBL:X05021; NID:g36807; PIDN:CAA28691.1; PID:g36808

R:Veilleux, A.; Foss, F.M.; Sauvillie, E.A.; Bolen, J.B.; Rosen, N.

Oncogene Res. 1, 357-374, 1987

A>Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other

A:Reference number: S01879; MUID:88217332; PMID:2835736

A:Accession: S01879

A:Molecule type: mRNA

A:Residues: 368-471, 'H', 473-509 <VEI>

A:Cross-references: EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID:g34289

R:Trevisan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Lima, T.J.

Biochim. Biophys. Acta 888, 286-295, 1986

A>Title: Human T lymphocytes express a protein-tyrosine kinase homologue to p56 (lck)

A:Reference number: S07143; MUID:87000726; PMID:3489486

A:Accession: S07143

A:Molecule type: mRNA

A:Residues: A, 378-509 <TRB>

A:Cross-references: EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID:g35780

R:Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W.

Mol. Cell. Biol. 9, 2173-2180, 1989

A>Title: Structure of the two promoters of the human lck gene: differential accumulation

A:Reference number: A32797; MUID:89133644; PMID:2787474

A:Accession: A32797

A:Molecule type: DNA

A:Residues: 1-35 <TRK>

A:Cross-references: GB:M26692; NID:g341533; PIDN:AAA59503.1; PID:g349702

R:Garvin, A.M.; Pawar, S.; March, J.D.; Perlmuter, R.M.

Mol. Cell. Biol. 8, 3058-3064, 1988

A>Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell

A:Reference number: 157636; MUID:89096691; PMID:2850479

A:Accession: 157636

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-35, VR, <RES>

A:Cross-references: GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:g553522

C:Comment: Protein tyrosine kinases play important roles in the control of cell growth

C:Gene: GDB:LCK

A:Cross-references: GDB:119360; OMTM:153390

A:Map position: 1p35-1p34.3

A:Insertions: 35/3; 63/1; 93/2; 126/2; 161/1; 262/1; 322/1; 347/3; 399/1; 443/1

C:Function:

A:Description: catalyzes the phosphorylation of a peptide tyrosine residue by ATP

C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pnc

F:2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>

F:168-116/Domain: SH3 homology <SH3>

F:127-224/Domain: SH2 homology <SH2>

F:224-501/Domain: protein kinase homology <KIN>

F:251-259/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:3.5/Binding site: palmitate (Cys) (covalent) #status predicted

F:273/Active site: Lys #status predicted

F:394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 25.5%; Score 344; DB 1; Length 509;

Best Local Similarity 41.1%; Pred. No. 1.4e-20;

Matches 74; Conservative 26; Mismatches 70; Indels 10; Gaps 2;

Qy 26 VTMEERSKAT-----AVAGSPAGPAELSLRLGEPLTIVSEGDPMWTVLSEVSGRE 79

Db 49 VTVEGSPAPSLQDNLVIALHSYPSHSDGLGEGEQLRLFGSGGPMWASLTTGGE 108

Qy 80 YNIPSVHVAKVS-----HGMVLEGLSRKAEELLLDGNCGAFILRSQTRRSYSLRSLR 135

Db 109 GRPFPNPAKANSLEPEPEFKNLSRCDAROLLAAQNHGHSFLLRSESTAGSSLSLR 168
 QY 136 LSPPASMDRIRRHRIHCLDNGMLYISPLTFPSQLVDHISELADIDICLLKEPCVQR 195
 Db 169 DFDQNGSVVAKYKIRNLDNGGFYISPLTFPSQLVDHISELADIDICLLKEPCVQR 228

RESULT 11

148845
 protein-tyrosine kinase (EC 2.7.1.112) lck lymphocyte - mouse

N/Alternate names: p56; protein-tyrosine kinase cck

C/Species: Mus musculus (house mouse)

C/Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 03-Mar-2000

C/Accession: 148845; A23639; I57629; I77452

R/Voronova, A. F.; Sefton, B. M.

Nature 319, 682-685, 1986

A/Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote

A/Reference number: 148845; PMID:86146842; PMID:3081813

A/Accession: 148845

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-509 <VOR1>

A/Cross-references: EMBL:X03533; NID:954813; PIDN:CAA27234.1; PID:954814

R/Marth, J. D.; Peet, R.; Krebs, E. G.; Perlmutter, R. M.

Cell 43, 393-404, 1985

A/Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpress

A/Reference number: A23639; PMID:86079521; PMID:2416464

A/Accession: A23639

A/Molecule type: mRNA

A/Residues: 1-282; 'VP', 285-509 <MAR>

A/Cross-references: GB:M12056; NID:9198763

A/Note: the sequence is revised in GenBank entry MUSLCK, release 116.0, (PIDN:AAB59674.1

R/Voronova, A. F.; Adler, H. T.; Sefton, B. M.

Mol. Cell. Biol. 7, 4407-4413, 1987

A/Title: Two lck transcripts containing different 5' untranslated regions are present in

A/Reference number: I57629; PMID:86142832; PMID:3501824

A/Accession: I57629

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-11 <VOR>

A/Cross-references: GB:M18098; NID:9198766; PIDN:AAA39422.1; PID:9198767

R/Garvin, A. M.; Pawar, S.; Marth, J. D.; Perlmutter, R. M.

Mol. Cell. Biol. 8, 3058-3064, 1988

A/Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell

A/Reference number: I57636; PMID:89096891; PMID:2850479

A/Accession: I77452

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-35; 'VR', <GAR>

A/Cross-references: GB:M21511; NID:9198768; PIDN:AAA39422.1; PID:9554186

C/KeyWords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro

F/68-116/Domain: SH3 homology <SH3>

F/127-224/Domain: SH2 homology <SH2>

F/243-501/Domain: protein kinase homology <KIN>

F/251-259/Region: protein kinase ATP-binding motif

F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F/237/Active site: Lys #status predicted

F/394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 35.4%; Score 342.5; DB 1; Length 509;

Best Local Similarity 39.6%; Pred. No. 1.8e-20;

Matches 78; Conservative 28; Mismatches 84; Indels 7; Gaps 2;

QY 3 SLPSRRKSLPSPLSSSVQGGPVTEARSKATAVAVLGFPAAGPAELSLRLGEPLTIV 62

Db 35 SLPIRNGSEVRDPL--VTYEGSLPASPDLQNVIALHSEYSHDGLGFEKEQRLIL 91

QY 63 SEDGDWWTYLSVSGREYINPVSVAKVS---HGMVLEGLSEKSEKELLILPPNPGAP 118

Db 92 EQSGEWMKQSLTGGEGFIPENFVAKANSLEPEPEFKNLSRCDAROLLAAQNHGHSF 151

QY 119 LIRESGRGSYSLSVRLSPASMDRIRRHRIHCLDNGMLYISPLTFPSQLVDHISELADIDICLLKEPCVQR 178
 Db 152 LIRESGTASPSLSVRDQNGGVVAKYKIRNLDNGGFYISPLTFPSQLVDHISELADIDICLLKEPCVQR 211
 QY 179 LADICLLKEPCVQR 195
 Db 212 ASDGLCTKLSPFCQYOK 228

RESULT 12

A39939
 protein-tyrosine kinase (EC 2.7.1.112) tk1 [similarity] - chicken

N/Alternate names: kinase-related transforming protein (tk1); T-cell surface antigen aas

C/Species: Gallus gallus (chicken)

C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000

C/Accession: A42126; A39939

R/Chow, L. M.; Ratcliffe, M. J.; Veilleux, A.

Mol. Cell. Biol. 12, 1226-1233, 1992

A/Title: tk1 is the avian homolog of the mammalian lck tyrosine protein kinase gene.

A/Reference number: A42126; PMID:92186854; PMID:1545804

A/Accession: A42126

A/Molecule type: mRNA

A/Residues: 1-88 <CHO>

A/Cross-references: GB:M85043

A/Experimental source: thymus, spleen

A/Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBI:88833)

R/Strebhardt, K.; Mullins, J. I.; Bruck, C.; Ruesamen-Waigmann, H.

Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987

A/Title: Additional member of the protein-tyrosine kinase family: the src-and lck-relate

A/Reference number: A39939; PMID:86097370; PMID:3321053

A/Accession: A39939

A/Molecule type: mRNA

A/Residues: 52-507 <STR>

A/Cross-references: GB:J03579; NID:9212712; PIDN:AAA49081.1; PID:9212713

C/KeyWords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pnc

F/66-114/Domain: SH3 homology <SH3>

F/125-222/Domain: SH2 homology <SH2>

F/241-499/Domain: protein kinase homology <KIN>

F/249-257/Region: protein kinase ATP-binding motif

F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F/392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 24.9%; Score 337; DB 1; Length 507;

Best Local Similarity 43.8%; Pred. No. 5.1e-20;

Matches 71; Conservative 27; Mismatches 60; Indels 4; Gaps 1;

QY 38 VALGSPFAGPAPSLRLGEPLTIVSDGPMWTVLSEVSGREYINPVSVAKVS---HG 93

Db 65 VALDYEPYTHDGLKQGEKLRVBSGEMWRAQSLTGGEGILPNNFVAMNLSLEPEP 124

QY 94 WLYEGLSEKAEELLILPPNPGAFILRESQTRGSYSLSVRLSPASMDRIRRHRIHCL 153

Db 125 WFFKSLSKVAEARLLASGNTGSLIRESETSKGSYSLSVRDQNGGVVAKYKIRNM 184

QY 154 DNGWLYSPPLTFPSQLVDHISELADIDICLLKEPCVQR 195

Db 185 DNGGYISPRVTSLSLHEVLYSSSDGLCTKLGRCTYOK 226

RESULT 13

B49114
 protein-tyrosine kinase (EC 2.7.1.112) fyn - Pacific electric ray

C/Species: Torpedo californica (Pacific electric ray)

C/Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 18-Feb-2000

C/Accession: B49114

R/Swope, S. L.; Huganir, R. L.

J. Biol. Chem. 268, 25152-25161, 1993

A/Title: Molecular cloning of two abundant protein tyrosine kinases in Torpedo electric

A/Reference number: A49114; PMID:94043386; PMID:8227079

A/Accession: B49114

A/Status: preliminary

A/Molecule type: mRNA

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Db 171 IFLVRESEETKAYSLR-----DWDEVGDNVGHYKIKLNGGYITTPAQSLSIQK 225
Qy 172 LVVHYSELADDDICLLKRPC-----VLQRAQPLRGQIDILPTTVOR----- 212
Db 226 LVKHYHEHADGCHCLTTCVPTVKPOTQGLAKDAWEIPRESLSLEYKLDGQCGFGEVMNGT 285
Qy 213 ----TPLNWKEIDSSLLFSEPAATGESLSLSEGLRESL-SFYISLNDNAV 256
Db 286 WNGTTKVAIKTLKGTWMPPEAFLOEQAIMKKLRHDKLVPLVAVVSEEP1 314

RESULT 15
A45501
protein-tyrosine kinase (EC 2.7.1.112) yes [similarity] - African clawed frog
N/Alternate names: kinase-related transforming protein (yes)
C/Species: Xenopus laevis (African clawed frog)
C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000
C/Accession: A45501; S08517
R/Steale, R.E.; Iwata, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.
Oncogene Res. 1, 223-233, 1989
A/Title: The yes proto-oncogene is present in amphibians and contributes to the maternal
A/Reference number: A45501
A/Accession: A45501
A/Molecule type: mRNA
A/Residues: 1-537 <STE>
A/Cross-references: GB:X14377
R/Steale, R.E.; Iwata, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.
submitted to the EMBL Data Library, February 1989
A/Reference number: S08517
A/Accession: S08517
A/Molecule type: mRNA
A/Residues: 1-250/'S',252-537 <ST2>
A/Cross-references: EMBL:X14377; NID:965272; PIDD:CA32551.1; PID:965273
C/Genetics: yes
A/Name: yes
C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
C/Keywords: ATP autophosphorylation; blocked amino end; kinase-related transforming pr
F/192-141/Domain: SH3 homology <SH3>
F/152-249/Domain: SH2 homology <SH2>
F/169-527/Domain: protein kinase homology <KIN>
F/277-285/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/299/Active site: Lys #status predicted
F/420,531/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 23.9%; Score 323.5; DB 1; Length 537;
Best Local Similarity 33.6%; Pred. No.7.1e-19;
Matches 85; Conservative 38; Mismatches 91; Indels 39; Gaps 7;

Qy 38 VALGSPFAGDAELSLRLGEPRLTYS-DCGMWTVLSEVSGREYNIIPGVHAKV----SH 92
Db 91 VALVYEARTTEDTSPFKGERFQIINNEGDMWEARSIAATGKTYIPSNVVAAPDSIQAE 150
Qy 93 GMLVESELSEKAEELLPLGNPCGAFLRESQTRGYSLSVRLSPRSWPRIR-----H 147
Db 151 EMTFGMKGRKDERKLINPGRGFLVRESEETKAYSLR-----DWDEVGDNVGR 205
Qy 148 YRIHCLDGMWLYSPRLTFPSLQALVDHYSELADDDICLLKRPC-----VLQRAQ 198
Db 206 YKIRKLIDNGGYITTPAQSLSIQKLVKHYSEHADGCLCYRLTTCVPTVKPOTQGLAKDAWE 265
Qy 199 LPKQDLPPTVTVOR-----TPLNWKEIDSSLLFSEPAATGESLSLSEGLRES 244
Db 266 IPRESLRIDVTLGGCGCGEVMIGTWNGTTKVAIKTLKPGTWMPPEAFLOEQAIMKKLRHDK 325
Qy 245 L-SFYISLNDNAV 256
Db 326 LVPLVAVVSEEP1 338

Search completed: March 24, 2003, 15:51.36
Job time : 25.1455 secs

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